

RAW SEQUENCE LISTING DATE: 07/06/2000
PATENT APPLICATION: US/09/233,218A TIME: 13:06:42

Input Set : A:\Tetrapyrrole-15090-B.txt
Output Set: N:\CRF3\07062000\I233218A.raw

1 <110> APPLICANT: Cajacob, Claire A.
2 Liu, Jingdong
4 <120> TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
5 The Tetrapyrrole Pathway
7 <130> FILE REFERENCE: 38-21(15090)B
9 <140> CURRENT APPLICATION NUMBER: US 09/233,218A
10 <141> CURRENT FILING DATE: 1999-01-20
12 <150> PRIOR APPLICATION NUMBER: US 60/067,000
13 <151> PRIOR FILING DATE: 1998-11-24
14 <151> PRIOR APPLICATION NUMBER: US 60/069,472
15 <151> PRIOR FILING DATE: 1997-10-09
16 <151> PRIOR APPLICATION NUMBER: US 60/072,027
18 <151> PRIOR FILING DATE: 1998-01-21
21 <150> PRIOR APPLICATION NUMBER: US 60/074,201
22 <151> PRIOR FILING DATE: 1998-02-10
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70 <151> PRIOR FILING DATE: 1998-03-18
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ENTERED

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JUL 19 2000
TECH CENTER 1600/2900

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Input Set : A:\Tetrapyrrole-15090-B.txt
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76 <151> PRIOR FILING DATE: 1998-04-27
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 157 <151> PRIOR FILING DATE: 1998-09-22
 160 <151> PRIOR FILING DATE: 1998-10-13
 163 <151> PRIOR FILING DATE: 1998-10-13
 166 <151> PRIOR FILING DATE: 1998-11-18
 169 <151> PRIOR FILING DATE: 1998-11-18
 172 <151> PRIOR FILING DATE: 1998-11-24
 175 <151> PRIOR FILING DATE: 1998-12-01
 178 <151> PRIOR FILING DATE: 1998-12-11
 181 <160> PRIOR FILING DATE: 1998-12-22
 183 <160> NUMBER OF SEQ ID NOS: 677
 185 <210> SEQ ID NO: 1
 186 <211> LENGTH: 257
 187 <212> TYPE: DNA
 188 <213> ORGANISM: Glycine max
 190 <400> SEQUENCE: 1
 192 ttttgtttttt ggaaatttt atttttttt taaatgtttt gttttttttt 60
 194 gttttttttt tttttttttt tgacaggata taccaggactt atgtttttttt ggtttttttt 120
 196 tttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 180
 198 tttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 240
 200 gttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 257
 203 <210> SEQ ID NO: 2
 204 <211> LENGTH: 272

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Input Set : A:\Tetrapyrrole-15090-B.txt
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293 <210> SEQ ID NO: 7
 294 <211> LENGTH: 278
 295 <212> TYPE: DNA
 296 <213> ORGANISM: Glycine max
 298 <400> SEQUENCE: 7
 300 cggctcgag aagacacag aagggtctag agtactgtta ttgaaaggca aaggacaata 60
 302 gagatatactt gaaggccctag aggcctatcc ctctcaacac ttttgaatgc attgacaata 120
 304 gcaatccca actgtcaatg gatttaacaa caacatataa aaccattttt atttgacata 180
 306 ttatcatattt catatccaaac aaaaatgtcat gaagaatata ttacatactc cagctatgtct 240
 308 gtataga ttgtggaaacaa ttatatctgg ttgatggag 278
 311 <210> SEQ ID NO: 8
 312 <211> LENGTH: 248
 313 <212> TYPE: DNA
 314 <213> ORGANISM: Glycine max
 316 <400> SEQUENCE: 8
 318 cggctcgag aagacacag aagggtctag agtactgtta ttgaaaggca aaggacaata 60
 320 gagatatactt gaaggccctag aggcctatcc ctctcaacac ttttgaatgc attgacaata 120
 322 gcaatccca actgtcaatg gatttaacaa caacatataa aaccattttt atttgacata 180
 324 ttatcatattt catatccaaac aaaaatgtcat gaagaatata ttacatactc cagctatgtct 240
 326 gtataga 248
 329 <210> SEQ ID NO: 9
 330 <211> LENGTH: 258
 331 <212> TYPE: DNA
 332 <213> ORGANISM: Glycine max
 334 <223> OTHER INFORMATION: unsure at all n locations
 W--> 335 <400> SEQUENCE: 9
 W--> 337 gncancgtt angganccta ctnctactgg cngagggttt tgaacttgc cttnnnngaca 60
 W--> 339 aatctatctt ggcatttctcct cttctcgccg cngtggctng aggacttggaa haattnmcgag 120
 W--> 341 taccctttttt aggtttgtatn atctgttgtt cacaatgcag ggnacacaaa caratttggct 180
 W--> 343 ggttaatgtt cttccaaagge gaaaccttggn ggacttgggg ggacttcagg gtggtttgaa 240
 345 tggatgttgggg aggtttggc 258
 346 <210> SEQ ID NO: 10
 349 <211> LENGTH: 270
 350 <212> TYPE: DNA
 351 <213> ORGANISM: Glycine max
 353 <400> SEQUENCE: 10
 355 gtcaatttgt tgataactttt aggcacatccg gcccggccact ggatgtgttt gtttcaatgt 60
 357 ctgcgggtttt ctgcggccact gcccaggaaac ctacatatac tgcgtatggc ttggaaactca 120
 359 qtgttggaaac caaccatcttc gggcattttcc tcccttcgccc cttttgtttt gacyacttgg 180
 361 acaaaatctgtt ctacccttcg aacgggtttga tcatgttaggc tcaatccacag gaaacaccaa 240
 363 cacatgtgtt ggaatgtggcc accccaggctt 270
 366 <210> SEQ ID NO: 11
 367 <211> LENGTH: 258
 368 <212> TYPE: DNA
 369 <213> ORGANISM: Glycine max
 371 <223> OTHER INFORMATION: unsure at all n locations
 W--> 372 <400> SEQUENCE: 11
 374 cagaacaaac caacacatgg gctggaaatg tgccacccaa ggcttaacccctt ggtgacatga 60
 376 ggggacttgc tgagggtctt aatgggtctaa acatccggc catgtatgtt ggaggatctt 120

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Input Set: A:\Tetrapyrrole-15090-B.txt
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378 tttagccgc taatgcatac aaggacaga aagtctgc aaatgttata atgcaggaaat 180
 W--> 380 tcccaacagg gptccgcgtt ganacccnng nataacatnt gmcocctan cccgggtt 240
 W--> 382 ttccncccaaa agggnntt 258
 385 <210> SEQ ID NO: 12
 386 <211> LENGTH: 120
 387 <212> TYPE: DNA
 388 <213> ORGANISM: Glycine max
 390 <400> SEQUENCE: 12
 392 gacggccgtt aggcatcaaa ggacacggaa gctgtcaaca tgcttacaat gcaaggattc 60
 394 cacagaaatg accatgtatg acatgttgc ccctttaccg aggtgtatc 120
 396 gcccaacacg gtctgttgc agagcacatt cccgttgc gactttctt ccctccatc 180
 398 ccaaagtatc taatccaaaggg ttgttgc ta gaatgtatgatc caggaaagg acttgcacatc 240
 400 gtttgtaaatg atccaaaggat aacaaaatca 270
 403 <210> SEQ ID NO: 13
 404 <211> LENGTH: 262
 405 <212> TYPE: DNA
 406 <213> ORGANISM: Glycine max
 408 <400> SEQUENCE: 13
 410 caggctgtt ctttcccccatt tgctaaagg gggaaatgtc gtgtttctt caggatcccc 60
 412 acaaattgtc gtgtttcg atgtccgatct ctcaatatcg acgtctcaatg ttttcttcat 120
 414 gacatgcaaa gaaacaccaa cacccttgcg ggacatgtgc caccggcggc taacatgttgc 180
 416 gacttggaggc gactgttgc aggttgcgtt gggctttaaca cttcaggccat gatagatgg 240
 418 ggatcccttg atggcaccatc 262
 421 <210> SEQ ID NO: 14
 422 <211> LENGTH: 279
 423 <212> TYPE: DNA
 424 <213> ORGANISM: Glycine max
 426 <223> OTHER INFORMATION: unsure at all n locations
 W--> 427 <400> SEQUENCE: 14
 429 ccattgtctt cccttcccat cggatgtccat gccacaacag gcctgtccg agagcacatt 60
 W--> 430 cccctgttca naacttgcgtt ccctccatc cagaaggatca taaccaagg ctatgttctca 180
 432 gaaatgttgc cggaaatggc acgttgcgtt gttgtaaatg atccaaatct aacaaaatct 180
 435 gtgttactt ggaaatgtggc acgttgcgtt gttgttttgcg aaaatggatc 240
 W--> 437 cccttgcgttcc cggaaatggc acgttgcgtt gttgtaaatc tggggatgtt 279
 440 <210> SEQ ID NO: 15
 441 <211> LENGTH: 346
 442 <212> TYPE: DNA
 443 <213> ORGANISM: Glycine max
 445 <400> SEQUENCE: 15
 447 aaacaaatggc cccaggatca cattttttttt tttttttttt ttccaaatggc tttttttttt 60
 449 gttttttttt tttttttttt tttttttttt gttttttttt gttttttttt gttttttttt 120
 451 aaggacacccaa caatgttgcgtt tttttttttt tttttttttt tttttttttt 180
 453 cccttgcgttcc ctgtccaaatgg gttttttttt gttttttttt gttttttttt 240
 455 gtgtccaaatgg caacttcggc agttccaaatgg gttttttttt gttttttttt 300
 457 aaatggatgttcc ttatataatc tggggatgttcc tttttttttt tttttttttt 346
 460 <210> SEQ ID NO: 16
 461 <211> LENGTH: 256
 462 <212> TYPE: DNA
 463 <213> ORGANISM: Glycine max

J

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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 Input Set: A:\Tetrapyrrole-15090-B.txt
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L:69 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:72 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:75 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:78 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:81 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:84 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:87 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:90 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:93 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:96 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:99 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:102 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:105 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:108 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:111 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:114 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:117 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:120 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:123 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:126 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:129 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:132 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:135 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:138 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:141 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:144 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:147 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:150 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:153 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:156 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:159 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:162 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:165 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:168 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:171 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:174 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:177 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:180 M:259 W: Field exceeds allowed number of lines, 19 <150> PRIOR APPLICATION NUMBER
 L:209 M:283 W: Missing Blank Line separator, <400> field identifier
 L:213 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
 L:213 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
 L:213 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
 L:213 M:340 W: (46) "n" or "xaa" used: Feature required, for SEQ ID#:2
 L:262 M:283 W: Missing Blank Line separator, <400> field identifier
 L:264 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
 L:264 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
 L:264 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
 L:264 M:340 W: (46) "n" or "xaa" used: Feature required, for SEQ ID#:5

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Input Set : A:\Tetrapyrrole-15090-8.txt
 Output Set : N:\CRF3\07062000\I233218A.raw

L:266 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
 L:266 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
 L:266 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
 M:340 Repeated in SeqNo=5
 L:331 M:283 W: Missing Blank Line separator, <400> field identifier
 L:337 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9
 L:337 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
 L:337 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
 L:337 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
 L:339 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9
 L:339 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
 L:339 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
 L:340 M:258 W: Repeated in SeqNo=1
 L:341 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9
 L:341 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
 L:341 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
 L:343 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9
 L:343 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
 L:343 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
 L:372 M:283 W: Missing Blank Line separator, <400> field identifier
 L:380 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
 L:380 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
 L:380 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
 L:381 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
 L:382 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
 L:382 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
 L:382 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
 L:384 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
 L:384 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
 L:384 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
 M:340 Repeated in SeqNo=1
 L:431 M:283 W: Missing Blank Line separator, <400> field identifier
 L:431 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:14
 L:431 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:14
 L:431 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
 L:431 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14
 L:437 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:14
 L:437 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:14
 L:437 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
 M:340 Repeated in SeqNo=18
 L:502 M:283 W: Missing Blank Line separator, <400> field identifier
 L:502 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:18
 L:504 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18
 L:504 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18
 L:504 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
 L:514 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:18
 L:514 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18
 L:514 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18
 M:340 Repeated in SeqNo=18
 L:685 M:283 W: Missing Blank Line separator, <400> field identifier
 L:691 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:28
 L:691 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28

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L:691 M:258 W: Mandatory Feature missing, <22> not found for SEQ ID#:28
 L:691 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28
 L:693 M:258 W: Mandatory Feature missing, <22> not found for SEQ ID#:28
 L:693 M:258 W: Mandatory Feature missing, <22> not found for SEQ ID#:28
 L:693 M:258 W: Mandatory Feature missing, <22> not found for SEQ ID#:28
 M:340 Repeated in SeqNo=28
 L:695 M:258 W: Mandatory Feature missing, <22> not found for SEQ ID#:28
 L:695 M:258 W: Mandatory Feature missing, <22> not found for SEQ ID#:28
 L:695 M:258 W: Mandatory Feature missing, <22> not found for SEQ ID#:28
 L:701 M:283 W: Missing Blank Line separator, <400> field identifier
 L:704 M:258 W: Mandatory Feature missing, <22> not found for SEQ ID#:29
 L:706 M:258 W: Mandatory Feature missing, <22> not found for SEQ ID#:29
 L:706 M:258 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:29
 M:340 Repeated in SeqNo=29
 L:739 M:203 W: Missing Blank Line separator, <400> field identifier
 L:755 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:31
 L:782 M:283 W: Missing Blank Line separator, <400> field identifier
 L:790 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:33
 L:815 M:283 W: Missing Blank Line separator, <400> field identifier
 L:817 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:35
 L:834 M:283 W: Missing Blank Line separator, <400> field identifier
 L:834 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:36
 M:340 Repeated in SeqNo=36
 L:904 M:283 W: Missing Blank Line separator, <400> field identifier
 L:911 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:40
 L:926 M:283 W: Missing Blank Line separator, <400> field identifier
 L:930 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:41
 M:340 Repeated in SeqNo=41
 L:1033 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1041 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:47
 M:340 Repeated in SeqNo=47
 L:1124 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1132 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:52
 L:1143 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1145 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:53
 M:340 Repeated in SeqNo=53
 L:1162 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1164 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:54
 M:340 Repeated in SeqNo=54
 L:1339 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1341 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:64
 M:340 Repeated in SeqNo=64
 L:1376 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1378 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:66
 L:1505 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1509 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:73
 L:1568 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1572 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:77
 M:340 Repeated in SeqNo=77

VERIFICATION SUMMARY DATE: 07/06/2000
 PATENT APPLICATION: US/09/233,218A TIME: 13:06:43
 Input Set : A:\Tetrapyrrole-15090-B.txt
 Output Set: Ni\CRF3\07062000\I233218A.raw

L:1739 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1743 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:87
 M:340 Repeated in SeqNo=87
 L:1798 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1806 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:90
 L:1871 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1873 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:94
 L:1908 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1910 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:96
 M:340 Repeated in SeqNo=96
 L:1927 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1929 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:97
 M:340 Repeated in SeqNo=97
 L:1974 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1976 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:100
 M:340 Repeated in SeqNo=100
 L:2063 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2065 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:105
 M:340 Repeated in SeqNo=105
 L:2210 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2212 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:113
 M:340 Repeated in SeqNo=113
 L:2347 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2384 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2421 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2452 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2483 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2554 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2559 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2632 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2711 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2830 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2925 M:283 W: Missing Blank Line separator, <400> field identifier
 L:3016 M:283 W: Missing Blank Line separator, <400> field identifier
 L:3035 M:283 W: Missing Blank Line separator, <400> field identifier
 L:3152 M:283 W: Missing Blank Line separator, <400> field identifier
 L:3171 M:283 W: Missing Blank Line separator, <400> field identifier
 L:3282 M:283 W: Missing Blank Line separator, <400> field identifier
 L:3317 M:283 W: Missing Blank Line separator, <400> field identifier
 L:3406 M:283 W: Missing Blank Line separator, <400> field identifier
 L:3445 M:283 W: Missing Blank Line separator, <400> field identifier
 L:3610 M:283 W: Missing Blank Line separator, <400> field identifier